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SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: WAHL, DR., GEOFFREY M.
O'GORMAN DR., STEPHEN V.
- (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
(B) STREET: 444 South Flower Street, Suite 2000
(C) CITY: Los Angeles
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/666,252
(B) FILING DATE: 08-MAR-1991
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: REITER MR., STEPHEN E.
(B) REGISTRATION NUMBER: 31192
(C) REFERENCE/DOCKET NUMBER: P31 8929
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (619) 535-9001
(B) TELEFAX: (619) 535-8949

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
 (B) CLONE: NATIVE FLP

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 48
 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
 1 5 10 15

CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA 96
 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
 20 25 30

TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC 144
 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
 35 40 45

GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 192
 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
 50 55 60

AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 240
 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
 65 70 75 80

TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 288
 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
 85 90 95

ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT 336
 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
 100 105 110

CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA 384
 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
 115 120 125

TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT 432
 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
 130 135 140

AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA 480
 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
 145 150 155 160

ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT 528
 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
 165 170 175

TTA Leu	TAC Tyr	CAA Gln	TTC Phe 180	CTC Leu	TTC Phe	CTA Leu	GCT Ala	ACT Thr 185	TTC Phe	ATC Ile	AAT Asn	TGT Cys	GGA Gly 190	AGA Arg	TTC Phe	576
AGC Ser	GAT Asp	ATT Ile 195	AAG Lys	AAC Asn	GTT Val	GAT Asp	CCG Pro 200	AAA Lys	TCA Ser	TTT Phe	AAA Lys	TTA Leu 205	GTC Val	CAA Gln	AAT Asn	624
AAG Lys	TAT Tyr 210	CTG Leu	GGA Gly	GTA Val	ATA Ile	ATC Ile 215	CAG Gln	TGT Cys	TTA Leu	GTG Val	ACA Thr 220	GAG Glu	ACA Thr	AAG Lys	ACA Thr	672
AGC Ser 225	GTT Val	AGT Ser	AGG Arg	CAC His	ATA Ile 230	TAC Tyr	TTC Phe	TTT Phe	AGC Ser	GCA Ala 235	AGG Arg	GGT Gly	AGG Arg	ATC Ile	GAT Asp 240	720
CCA Pro	CTT Leu	GTA Val	TAT Tyr	TTG Leu 245	GAT Asp	GAA Glu	TTT Phe	TTG Leu	AGG Arg 250	AAT Asn	TCT Ser	GAA Glu	CCA Pro	GTC Val 255	CTA Leu	768
AAA Lys	CGA Arg	GTA Val	AAT Asn 260	AGG Arg	ACC Thr	GGC Gly	AAT Asn 265	TCT Ser	TCA Ser	AGC Ser	AAT Asn	AAA Lys 270	CAG Gln	GAA Glu	TAC Tyr	816
CAA Gln	TTA Leu	TTA Leu 275	AAA Lys	GAT Asp	AAC Asn	TTA Leu	GTC Val 280	AGA Arg	TCG Ser	TAC Tyr	AAT Asn	AAA Lys 285	GCT Ala	TTG Leu	AAG Lys	864
AAA Lys 290	AAT Asn	GCG Ala	CCT Pro	TAT Tyr	TCA Ser	ATC Ile 295	TTT Phe	GCT Ala	ATA Ile	AAA Lys	AAT Asn 300	GGC Gly	CCA Pro	AAA Lys	TCT Ser	912
CAC His 305	ATT Ile	GGA Gly	AGA Arg	CAT His	TTG Leu 310	ATG Met	ACC Thr	TCA Ser	TTT Phe	CTT Leu 315	TCA Ser	ATG Met	AAG Lys	GGC Gly	CTA Leu 320	960
ACG Thr	GAG Glu	TTG Leu	ACT Thr	AAT Asn 325	GTT Val	GTG Val	GGA Gly	AAT Asn 330	TGG Ser	AGC Ser	GAT Asp	AAG Lys	CGT Arg	GCT Ala 335	TCT Ser	1008
GCC Ala	GTG Val	GCC Ala	AGG Arg 340	ACA Thr	ACG Thr	TAT Tyr	ACT Thr	CAT His 345	CAG Gln	ATA Ile	ACA Thr	GCA Ala	ATA Ile 350	CCT Pro	GAT Asp	1056
CAC His	TAC Tyr	TTC Phe 355	GCA Ala	CTA Leu	GTT Val	TCT Ser	CGG Arg 360	TAC Tyr	TAT Tyr	GCA Ala	TAT Tyr	GAT Asp 365	CCA Pro	ATA Ile	TCA Ser	1104
AAG Lys 370	GAA Glu	ATG Met	ATA Ile	GCA Ala	TTG Leu	AAG Lys 375	GAT Asp	GAG Glu	ACT Thr	AAT Asn	CCA Pro 380	ATT Ile	GAG Glu	GAG Glu	TGG Trp	1152
CAG Gln 385	CAT His	ATA Ile	GAA Glu	CAG Gln	CTA Leu 390	AAG Lys	GGT Gly	AGT Ser	GCT Ala	GAA Glu 395	GGA Gly	AGC Ser	ATA Ile	CGA Arg	TAC Tyr 400	1200
CCC Pro	GCA Ala	TGG Trp	AAT Asn	GGG Gly 405	ATA Ile	ATA Ile	TCA Ser	CAG Gln	GAG Glu 410	GTA Val	CTA Leu	GAC Asp	TAC Tyr	CTT Leu 415	TCA Ser	1248
TCC Ser	TAC Tyr	ATA Ile	AAT Asn 420	AGA Arg	CGC Arg	ATA Ile	TAAGTACGCA TTTAAGCATA AACACGCACT									1299

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ATGCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA 1359
ACAGTGAGCT GTATGTGCGC A 1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
1 5 10 15
Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
20 25 30
Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
35 40 45
Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
50 55 60
Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
65 70 75 80
Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
85 90 95
Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
100 105 110
Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
115 120 125
Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
130 135 140
Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
145 150 155 160
Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
165 170 175
Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
180 185 190
Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
195 200 205
Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
210 215 220
Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
225 230 235 240
Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
245 250 255
Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
260 265 270

Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
 275 280
 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
 290 295 300
 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
 305 310 315 320
 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
 325 330 335
 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
 340 345 350
 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
 355 360 365
 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
 370 375 380
 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
 385 390 395 400
 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
 405 410 415
 Ser Tyr Ile Asn Arg Arg Ile
 420

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: FLP recombination target site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG

60

GAACTTCA

68

Basil